knockdown of leech *hunchback* gene expression via splice-blocking antisense morpholino injection leads to gastrula defects similar to the knockdown phenotype observed in nematodes using RNA interference. Together these data suggest that hunchback-like proteins in lophotrochozoans and nematodes are important for normal morphogenesis to occur at gastrulation and that hunchback-like protein is expressed in feeding and locomotory structures in lophotrochozoa. Bioinformatic data suggest that the *hunchback* gene is restricted to the protostome lineage consistent with the hypothesis that deuterostome larvae are independently derived.

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Program/Abstract # 84
Function and phylogenetics of the NR2E nuclear receptors in *C. elegans*
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The NR2E subclass of nuclear receptors is conserved from cnidarians to vertebrates. Family members such as *tailless* and *fax-1* have been shown to function in nervous system development and body patterning. Phylogenetic analysis identifies at least three major clades of NR2E-related nuclear receptors: the NR2E1/2 clade, which includes *tailless*; the NR2E3/5 clade, which includes *fax-1*; and a new group that may represent one or two clades, including *nhr-239* of *Caenorhabditis* and related genes in insects and the echinoderm *Stongylocentrus*. The existence of a possible *nhr-239* ortholog in both protostomes and deuterostomes suggests that this class could have an ancient origin. While ligand-binding domains (LBD's) of nuclear receptors in insects and vertebrates share modest sequence similarity, the *Caenorhabditis* LBD's are considerably more diverged. The *nhr-111* gene, which is present in *C. elegans* but not *C. briggsae*, includes a *fax-1*-related LBD. We have used a gene fusion approach to show that LBD function is interchangeable among *C. elegans fax-1*, *C. briggsae fax-1* and *C. elegans nhr-111*. These data demonstrate that LBD function may be conserved among some nematode nuclear receptors, despite relatively low sequence conservation. Models support structural conservation of *Caenorhabditis* LBD's with vertebrate nuclear receptors. Deletions of *nhr-111* or *nhr-239* cause no obvious phenotype, suggesting that both perform subtle or redundant functions. *nhr-111* is expressed in some neurons and the somatic gonad precursor cells. We are exploring possible roles for *nhr-111* and *nhr-239* in behavior and development.

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Program/Abstract # 85
A novel Pax gene controls the formation of stem cells in the leech embryo
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We have cloned two members of a new subclass of Pax genes from the leech, *Helobdella* sp. (Austin). This Paxβ subfamily, is characterized by the presence of 10 unique residues in the paired domain, and is restricted to animals of the clade Lophotrochozoa. Using microinjection of mRNA for a fusion of one of these genes, *Hau-Paxβ1*, to the *engrailed* repressor (EnR) domain, we show that *Hau-Paxβ1* plays an important role in the future development of the ectodermal progenitor cell, DNOPQ‴. Normally, this cell undergoes several largely symmetric divisions to produce a set of eight teloblasts, each of which then initiates a program of highly asymmetric stem cell divisions. However, in the presence of Paxβ1-EnR, DNOPQ‴ undergoes at most one symmetric cell division, and then begins asymmetric stem cell divisions precociously. We therefore propose that the Hau-Paxβ1 protein is required for the transcription of gene product(s) that regulate the transformation of cleavage blastomeres into embryonic stem cells.

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Program/Abstract # 86
Function of vascular endothelial growth factor receptor of cephalopod, *Idiosepius paradoxus*
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Vascular endothelial growth factors (VEGFs) are the major inducers of vascular development and regulation of permeability of blood vessels in vertebrates. Their effects are mediated by tyrosine kinase receptors of the VEGF receptor (VEGFR) family. We cloned a VEGFR-like tyrosine kinase receptor from the pygmy-squid *Idiosepius paradoxus*, using RACE method. Vertebrate VEGFRs have seven immunoglobulin (Ig) domains in the extracellular region and a split-type tyrosine kinase domain in the intracellular region. Using the protein blast the intracellular tyrosine kinase domain of the *Idiosepius* VEGFR showed a homology to *Branchiostoma* VEGFR-like (E=1e-62) and *Gallus* VEGFR3/FLT4 (E=5e-59), but six Ig domains existed in their extracellular region. Expression patterns of the VEGFR gene were studied by whole mount *in situ* hybridization. The VEGFR gene was expressed in the developing heart and the vena cava in *Idiosepius* embryos. Subsequently, VEGFR was expressed in blood vessels of their arms, and the regions adjacent to optic lobes. The expression patterns suggest that the gene is involved in blood island formation. In mollusks the cephalopods have closed blood-vascular systems. However, the circulatory system appears to derive from an open blood-vascular system of a molluscan ancestor. This expression pattern of VEGFR is probably associated with unique circulatory systems in cephalopods.

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Program/Abstract # 87
Molecular characterization of pea aphid facultative parthenogenesis
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Meiosis is a highly conserved process in which a diploid genome is recombined and assorted into haploid gametes. Remarkably, the pea aphid *Acyrthosiphon pisum* exhibits a reproductive polyphenism whereby environmental signals trigger a switch between apomixis (parthenogenetic reproduction) and meiosis (sexual reproduction). Aphid apomixis results in daughter embryo clones with 2n genome content without male contribution or recombination. This important adaptation allows aphid populations to not only rapidly expand upon